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RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/10/067,385

TIME: 13:39:31

Input Set : A:\SP130.txt

Output Set: N:\CRF3\02262002\J067385.raw

4 <110> APPLICANT: Adamou, John
 5 Choi, Gil
 7 <120> TITLE OF INVENTION: Streptococcus Pneumoniae Proteins and Vaccines
 9 <130> FILE REFERENCE: 469201-589
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/067,385
 C--> 12 <141> CURRENT FILING DATE: 2002-02-05
 14 <150> PRIOR APPLICATION NUMBER: US/09/590,991
 15 <151> PRIOR FILING DATE: 2000-06-09
 17 <150> PRIOR APPLICATION NUMBER: US/60/138,453
 18 <151> PRIOR FILING DATE: 1999-06-10
 20 <160> NUMBER OF SEQ ID NOS: 8
 22 <170> SOFTWARE: PatentIn Ver. 2.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 21
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Description of Artificial Sequence: Forward primer
 31 for PCR amplification of Sp128 genomic sequences
 33 <400> SEQUENCE: 1
 34 taccggtag tcttagcaga c 21
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 25
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Artificial Sequence: Reverse primer
 43 for PCR amplification of Sp128 genomic sequence
 45 <400> SEQUENCE: 2
 46 atagccataa gttgattgc catta 25
 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 21
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial Sequence
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: Description of Artificial Sequence: Forward primer
 55 for PCR amplification of Sp130 genomic sequence
 57 <400> SEQUENCE: 3
 58 aagcttggcg agattgcaga a 21
 60 <210> SEQ ID NO: 4
 61 <211> LENGTH: 27
 62 <212> TYPE: DNA
 63 <213> ORGANISM: Artificial Sequence

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65 <220> FEATURE:
66 <223> OTHER INFORMATION: Description of Artificial Sequence: Reverse primer
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72 <210> SEQ ID NO: 5
73 <211> LENGTH: 1992
74 <212> TYPE: DNA
75 <213> ORGANISM: Streptococcus pneumoniae
77 <400> SEQUENCE: 5
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79 gaaaaagtag cagaaaaataa agagaaacat gaaaatatcc atagtgtctat ggaaacttca 120
80 caggattttta aagagaagaa aacagcagtc attaaggaaa aagaagttgt tagtaaaaaat 180
81 cctgtgatag acaataacac tagcaatgaa gaagcaaaaa tcaaagaaga aaattccaat 240
82 aaatcccaag gagattatac ggactcattt gtgaataaaa acacagaaaaa tccccaaaaa 300
83 gaagataaag ttgtctatat tgctgaattt aaagataaag aatctggaga aaaagcaatc 360
84 aaggaactat ccagtcttaa gaatacaaaa gttttatata cttatgatag aatttttaac 420
85 ggtagtgcca tagaaacaac tccagataac ttggacaaaa ttaacaaat agaaggtatt 480
86 tcatcggttg aaagggcaca aaaagtccaa cccatgatga atcatgccag aaaggaaatt 540
87 ggagttgagg aagctattga ttacctaaag tctatcaatg ctccgtttgg gaaaaatttt 600
88 gatgtagag gtatggtcac ttcaaatatc gatactggaa cagattatag acataaggct 660
89 atgagaatcg atgatgatgc caaagcctca atgagattta aaaaagaaga cttaaaaggc 720
90 actgataaaa attattggtt gagtgataaa atccctcatg cgttcaatta ttataatggt 780
91 ggcaaaatca ctgtagaaaa atatgatgat ggaagggatt attttgaccc acatgggatg 840
92 catattgcag ggattcttgc tggaaatgat actgaacaag acatcaaaaaa ctttaacggc 900
93 atagatggaa ttgcacctaa tgcacaaatt ttctcttaca aaatgtattc tgacgcagga 960
94 tctgggtttg cgggtgatga aacaatgttt catgctattg aagattctat caaacacaac 1020
95 gttgatgttg ttctcggtatc atctgggttt acaggaacag gtctttagtg tgagaaatat 1080
96 tggcaagcta ttcgggcatt aagaaaagca ggcattccaa tggttgtcgc tacgggtaac 1140
97 tatgcgactt ctgcttcaag ttcttcatgg gatttagtag caaataatca tctgaaaatg 1200
98 accgacactg gaaatgtaac acgaactgca gcacatgaag atgcgatagc ggtcgcttct 1260
99 gctaaaaatc aaacagttga gtttgataaa gtttaacatag gtggagaaaag ttttaaatat 1320
100 agaaatatag gggccttttt cgataagagt aaaatcacaa caaatgaaga tggaaacaaa 1380
101 gtccttagta aattaaaatt tgtatatata ggcaaggggc aagaccaaga tttgataggt 1440
102 ttggatctta ggggcaaaat tgcagtaatg gatagaattt atacaaagga tttaaaaaat 1500
103 gcttttaaaa aagctatgga taagggtgca cgcgccatta tggttgtaaa tactgtaaat 1560
104 tactacaata gagataattg gacagagctt ccagctatgg gatatgaagc ggatgaaggt 1620
105 actaaaagtc aagtgttttc aatttcagga gatgatggtg taaagctatg gaacatgatt 1680
106 aatcctgata aaaaaactga agtcaaaaaga aataataaag aagattttta agataaattg 1740
107 gagcaatact atccaattga tatggaaagt ttaatticca acaaaccgaa tgtaggtgac 1800
108 gaaaaagaga ttgactttta gtttgcacct gacacagaca aagaactcta taaagaagat 1860
109 atcatcgctt cagcaggatc tacatcttgg gggccaagaa tagatttact tttaaaaccc 1920
110 gatgtttcag cacctggtaa aatatataaa tccacgctta atgttattaa tggcaaatca 1980
111 acttatggct at
112                                     1992
113 <210> SEQ ID NO: 6
114 <211> LENGTH: 664
115 <212> TYPE: PRT
116 <213> ORGANISM: Streptococcus pneumoniae
118 <400> SEQUENCE: 6

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119 Tyr Pro Val Val Leu Ala Asp Thr Ser Ser Ser Glu Asp Ala Leu Asn
120 1 5 10 15
122 Ile Ser Asp Lys Glu Lys Val Ala Glu Asn Lys Glu Lys His Glu Asn
123 20 25 30
125 Ile His Ser Ala Met Glu Thr Ser Gln Asp Phe Lys Glu Lys Lys Thr
126 35 40 45
128 Ala Val Ile Lys Glu Lys Glu Val Val Ser Lys Asn Pro Val Ile Asp
129 50 55 60
131 Asn Asn Thr Ser Asn Glu Ala Lys Ile Lys Glu Glu Asn Ser Asn
132 65 70 75 80
134 Lys Ser Gln Gly Asp Tyr Thr Asp Ser Phe Val Asn Lys Asn Thr Glu
135 85 90 95
137 Asn Pro Lys Lys Glu Asp Lys Val Val Tyr Ile Ala Glu Phe Lys Asp
138 100 105 110
140 Lys Glu Ser Gly Glu Lys Ala Ile Lys Glu Leu Ser Ser Leu Lys Asn
141 115 120 125
143 Thr Lys Val Leu Tyr Thr Tyr Asp Arg Ile Phe Asn Gly Ser Ala Ile
144 130 135 140
146 Glu Thr Thr Pro Asp Asn Leu Asp Lys Ile Lys Gln Ile Glu Gly Ile
147 145 150 155 160
149 Ser Ser Val Glu Arg Ala Gln Lys Val Gln Pro Met Met Asn His Ala
150 165 170 175
152 Arg Lys Glu Ile Gly Val Glu Glu Ala Ile Asp Tyr Leu Lys Ser Ile
153 180 185 190
155 Asn Ala Pro Phe Gly Lys Asn Phe Asp Gly Arg Gly Met Val Ile Ser
156 195 200 205
158 Asn Ile Asp Thr Gly Thr Asp Tyr Arg His Lys Ala Met Arg Ile Asp
159 210 215 220
161 Asp Asp Ala Lys Ala Ser Met Arg Phe Lys Lys Glu Asp Leu Lys Gly
162 225 230 235 240
164 Thr Asp Lys Asn Tyr Trp Leu Ser Asp Lys Ile Pro His Ala Phe Asn
165 245 250 255
167 Tyr Tyr Asn Gly Gly Lys Ile Thr Val Glu Lys Tyr Asp Asp Gly Arg
168 260 265 270
170 Asp Tyr Phe Asp Pro His Gly Met His Ile Ala Gly Ile Leu Ala Gly
171 275 280 285
173 Asn Asp Thr Glu Gln Asp Ile Lys Asn Phe Asn Gly Ile Asp Gly Ile
174 290 295 300
176 Ala Pro Asn Ala Gln Ile Phe Ser Tyr Lys Met Tyr Ser Asp Ala Gly
177 305 310 315 320
179 Ser Gly Phe Ala Gly Asp Glu Thr Met Phe His Ala Ile Glu Asp Ser
180 325 330 335
182 Ile Lys His Asn Val Asp Val Val Ser Val Ser Ser Gly Phe Thr Gly
183 340 345 350
185 Thr Gly Leu Val Gly Glu Lys Tyr Trp Gln Ala Ile Arg Ala Leu Arg
186 355 360 365
188 Lys Ala Gly Ile Pro Met Val Val Ala Thr Gly Asn Tyr Ala Thr Ser
189 370 375 380
191 Ala Ser Ser Ser Ser Trp Asp Leu Val Ala Asn Asn His Leu Lys Met

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192 385          390          395          400
194 Thr Asp Thr Gly Asn Val Thr Arg Thr Ala Ala His Glu Asp Ala Ile
195          405          410          415
197 Ala Val Ala Ser Ala Lys Asn Gln Thr Val Glu Phe Asp Lys Val Asn
198          420          425          430
200 Ile Gly Gly Glu Ser Phe Lys Tyr Arg Asn Ile Gly Ala Phe Phe Asp
201          435          440          445
203 Lys Ser Lys Ile Thr Thr Asn Glu Asp Gly Thr Lys Ala Pro Ser Lys
204          450          455          460
206 Leu Lys Phe Val Tyr Ile Gly Lys Gly Gln Asp Gln Asp Leu Ile Gly
207 465          470          475          480
209 Leu Asp Leu Arg Gly Lys Ile Ala Val Met Asp Arg Ile Tyr Thr Lys
210          485          490          495
212 Asp Leu Lys Asn Ala Phe Lys Lys Ala Met Asp Lys Gly Ala Arg Ala
213          500          505          510
215 Ile Met Val Val Asn Thr Val Asn Tyr Tyr Asn Arg Asp Asn Trp Thr
216          515          520          525
218 Glu Leu Pro Ala Met Gly Tyr Glu Ala Asp Glu Gly Thr Lys Ser Gln
219          530          535          540
221 Val Phe Ser Ile Ser Gly Asp Asp Gly Val Lys Leu Trp Asn Met Ile
222 545          550          555          560
224 Asn Pro Asp Lys Lys Thr Glu Val Lys Arg Asn Asn Lys Glu Asp Phe
225          565          570          575
227 Lys Asp Lys Leu Glu Gln Tyr Tyr Pro Ile Asp Met Glu Ser Phe Asn
228          580          585          590
230 Ser Asn Lys Pro Asn Val Gly Asp Glu Lys Glu Ile Asp Phe Lys Phe
231          595          600          605
233 Ala Pro Asp Thr Asp Lys Glu Leu Tyr Lys Glu Asp Ile Ile Val Pro
234          610          615          620
236 Ala Gly Ser Thr Ser Trp Gly Pro Arg Ile Asp Leu Leu Leu Lys Pro
237 625          630          635          640
239 Asp Val Ser Ala Pro Gly Lys Asn Ile Lys Ser Thr Leu Asn Val Ile
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243          660
246 <210> SEQ ID NO: 7
247 <211> LENGTH: 2319
248 <212> TYPE: DNA
249 <213> ORGANISM: Streptococcus pneumoniae
251 <400> SEQUENCE: 7
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254 gaaaaatcta gttttactat tgatagaaat atttcaacaa ttagagactt tgaaaataaa 180
255 gacttaaaga aactcattaa aaagaaattt agagaagttg atgattttac aagtgaaact 240
256 ggtaagagaa tggaggaata cgattataaa tacgatgata aaggaaatat aatagcctac 300
257 gatgatggga ctgatctaga atatgaaact gagaaacttg acgaaatcaa atcaaaaatt 360
258 tatggtgttc taagtccgtc taaagatgga cactttgaaa ttcttggaaa gataagtaat 420
259 gtttctaaaa atgccaaagg atattatggg aataactata aatctataga aatcaaagcg 480
260 accaagtatg atttccactc aaaaacgatg acatttgatc tatacgctaa tattaatgat 540

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261 attgtggatg gattagcttt tgcaggagat atgagattat ttgttaaaga taatgatcag 600
262 aaaaaagctg aaattaaaaat tagaatgcct gaaaaaatta aggaaactaa atcagaatat 660
263 ccctatgtat caagttatgg gaatgtcata gaattagggg aaggagatct ttcaaaaaaac 720
264 aaaccagaca atttaactaa aatggaatct ggtaaaatct attctgattc agaaaaacaa 780
265 caatatctgt taaaggataa tatcattcta agaaaaggct atgcactaaa agtgactacc 840
266 tataatcctg gaaaaacgga tatgttagaa ggaaatggag tctatagcaa ggaagatata 900
267 gcaaaaatac aaaaaggccaa tcctaactcta agagcccttt cagaaacaac aatttatgct 960
268 gatagtagaa atgttgaaaga tggaagaagt acccaatctg tattaatgtc ggctttggac 1020
269 ggctttaaca ttataaggta tcaagtgttt acatttaaaa tgaacgataa aggggaagct 1080
270 atcgataaag acggaaatct tgtgacagat tcttctaaac ttgtattatt tggttaaggat 1140
271 gataaagaat acactggaga ggataagttc aatgtagaag ctataaaaga agatggctcc 1200
272 atgtttattta ttgataccaa accagttaac ctttcaatgg ataagaacta ctttaatcca 1260
273 tctaaatcta ataaaattta tgtacgaaat ccagaatttt atttaagagg taagatttct 1320
274 gataaggggtg gttttaactg ggaattgaga gttaatgaat cggttgtaga taattattta 1380
275 atctacggag atttacacat tgataacact agagatttta atattaagct gaatgttaaa 1440
276 gacggtgaca tcatggactg gggaatgaaa gactataaag caaacggatt tccagataag 1500
277 gtaacagata tggatggaaa tgtttatctt caaactggct atagcgattt gaatgctaaa 1560
278 gcagttggag tccactatca gtttttatat gataatgtta aaccggaagt aaacattgat 1620
279 cctaagggaa atactagtat cgaatatgct gatggaaaat ctgtagtctt taacatcaat 1680
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281 aaagaatata catcatttaa tgatatttaa caaataatag acaagacact aaacattaag 1800
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283 acgggagagg taagtgaatt aaaacctcat agggtaactg tgaccattca aaatggaaaa 1920
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286 gctggctatg ttattaatct atcaaaagat acctttataa aacctgtatt caagaaaata 2100
287 gaggagaaaa aggaggaaga aaataaacct acttttgatg tatcgaaaaa gaaagataac 2160
288 ccacaagtaa accatagtca attaaatgaa agtcacagaa aagaggattt acaaagagaa 2220
289 gagcattcac aaaaatctga ttcaactaag gatgttacag ctacagttct tgataaaaaa 2280
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292 <210> SEQ ID NO: 8

293 <211> LENGTH: 773

294 <212> TYPE: PRT

295 <213> ORGANISM: Streptococcus pneumoniae

297 <400> SEQUENCE: 8

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302           20           25           30
304 Gln Glu Asn Glu Glu Ser Ile Lys Glu Lys Ser Ser Phe Thr Ile Asp
305           35           40           45
307 Arg Asn Ile Ser Thr Ile Arg Asp Phe Glu Asn Lys Asp Leu Lys Lys
308           50           55           60
310 Leu Ile Lys Lys Lys Phe Arg Glu Val Asp Asp Phe Thr Ser Glu Thr
311   65           70           75           80
313 Gly Lys Arg Met Glu Glu Tyr Asp Tyr Lys Tyr Asp Asp Lys Gly Asn
314           85           90           95
316 Ile Ile Ala Tyr Asp Asp Gly Thr Asp Leu Glu Tyr Glu Thr Glu Lys
317           100          105          110

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date